

FIG. 1A Structural motifs in GRBP2

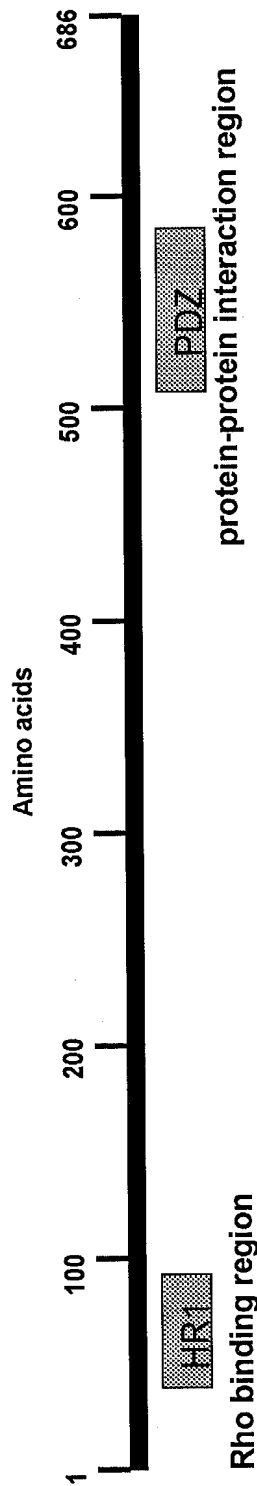


Fig. 1B HR1 domains

	10	20	30	40	50	60
consensus*.....*.....*.....*.....					
GRBP2	1 LLERLRKKLEVEIKTREGAEKILRLTSNEKV-----KRAKSEAIEKL--SNQKIEEL	52				
gi 7503594	38 ngraaINQQILKAVRMRI GAENLLKVA TNSKV-----REQVRL E--LSF--VNSDIQML	87				
gi 6093970	159 SKLVILQLELEKELKVKRGLEQFIRGAPDKS-----KVHGD S QSLDD--SRAKIAML	209				
gi 543444	42 SHRARLHQQISKELRMRTGAENLYRATSNVW-----RETVALELSYV-----NSNLQLL	91				
gi 6319363	216 LRFEELRHFRVHVAEAGAKNVRLLSAaK-----PDRKAYSEAQEKLTESNQKIGLL	270				
gi 6225859	5 QLEQNKKKTAVEENIIRGASALKKKTSNVW-----IQKCNINREA-----RQNLEYL	54				
gi 1085218	47 DIKDRIKREIRKELKIKEGAENLRKVTIDKK-----SLAYVDNLIK--SNKKIEEL	96				
gi 1175418	42 VERDRLRKEISRELKIKEGAENLRATTERK-----NLGHVETMLWT--CERRLES	91				
	38 KLEEDIKGKLEVECKIRDGAEFTLLQVDFTFKketkerKEMLKKKCTDELesSKKIEEL	97				

	70
consensus*.....
GRBP2	53 KQSL E-RLKELH 63
gi 7503594	88 KEEL E-GINisv 98
gi 6093970	210 RMQIE-RLSQEA 220
gi 543444	92 KEEL A-ELSTSV 102
gi 6319363	271 RESLE-RI GELP 282
gi 6225859	55 EDSL K-KIRLKT 65
gi 1085218	97 HHKL Q-EINAH I 107
gi 1175418	92 KQEL D-GLETPP 102
	98 VSSIE-SFOQEN 108

Fig. 1C PDZ domains

	10	20	30	40	50	60
consensus*.....*.....*.....*.....					
GRBP2	1 EPRIVELEKGG-----GGIGFSLVGGKDSGD-----GGVVVSVVPSPAAKAG- 44					
gi 13096475	513 PPRSIRFTAE-----GDLGFTLRGNA-----PVQHFIDPYCSASVAG- 551					
gi 7512038	70 PSRLAALRRGTAGSVTGVGLEITYDGSG-----KDVVLTTPAPGPAEKAG- 116					
gi 6671754	405 EPRFISFOKE-----GSVIRLTGGN-----EAGIFVTAVQPGSPASLQG- 444					
gi 7662086	484 EPTVEIIRLs-----DALGISIAGGKSPlg-----dIFIAMIQANGVAARTQk 531					
gi 131530	44 VQRCVIIQKQ-----HGFGFTVSGD-----RVLVQSVRPPGGAAMKAG- 82					
gi 6093970	507 YLVLIIRITPDe-----dGKFGNLIKGGVDq-----KPELVVSRINPEPADTCip 551					
gi 7499828	497 LVGPVHMTGGE-----GGFGFTLRGD-----SPVLIAAVVPGQAESAG- 535					
gi 8247939	46 RPHVVKVKSE-----TGFGFNVKGQVSEGGqlrslngqlYaPQHVSAVLRRGAADQAG- 100					
	410 IHVTILHKEEG-----AGLGFSLAGGADlEn-----KVITVHRVFPNGLASQEGt 454					
	70	80	90	100		
consensus*.....*.....*.....*.....					
GRBP2	45 -LKPGDVILEVNG-TSVEGLTHLEAVDLKE-AGG-----KVTLTVLRGG 86					
gi 13096475	552 -AREGDYIVSIQL-VDCKWLTLEVMKLIKsfGED-----ETEMKVVs11 594					
gi 7512038	117 -ARAGDVIVTDG-TAVKGLSLYDVSDLIQG-EADs---QVEWVLHAPG 159					
gi 6671754	445 -LMPGDKILKVN-DMDMGVTRREAVFLILs-LQD-----RIDLIQYCK 486					
gi 7662086	532 -LKVGDRIVSING-OPLDGLSHTDANLKN-AFG-----RIILQVADT 573					
gi 131530	83 -VKEGDRIKNGtMVTNss-HLEVVKLIKsg-----ayVALTILGSS 123					
gi 6093970	552 kLNEGQIVLINGr-DISEHTDQVMFIKA-SREshsrELAIIVIRRA 598					
gi 7499828	536 -LKEGDYIVSVNG-OPCKWVKHLEVVTQLRS-MGEe---GVSILQVWSLL 578					
gi 8247939	101 -LKKGDRILEVNG-LNVEGSTHRKVDLIKNG-GGD-----ELTMIVISVE 142					
	455 -IQKGEVLSING-KSLKGTTHDALAILRQ-AREp---RQAVIVTRKl 497					

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PROTEIN 2

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FIG. 2
Genomic structure of human GRBP2

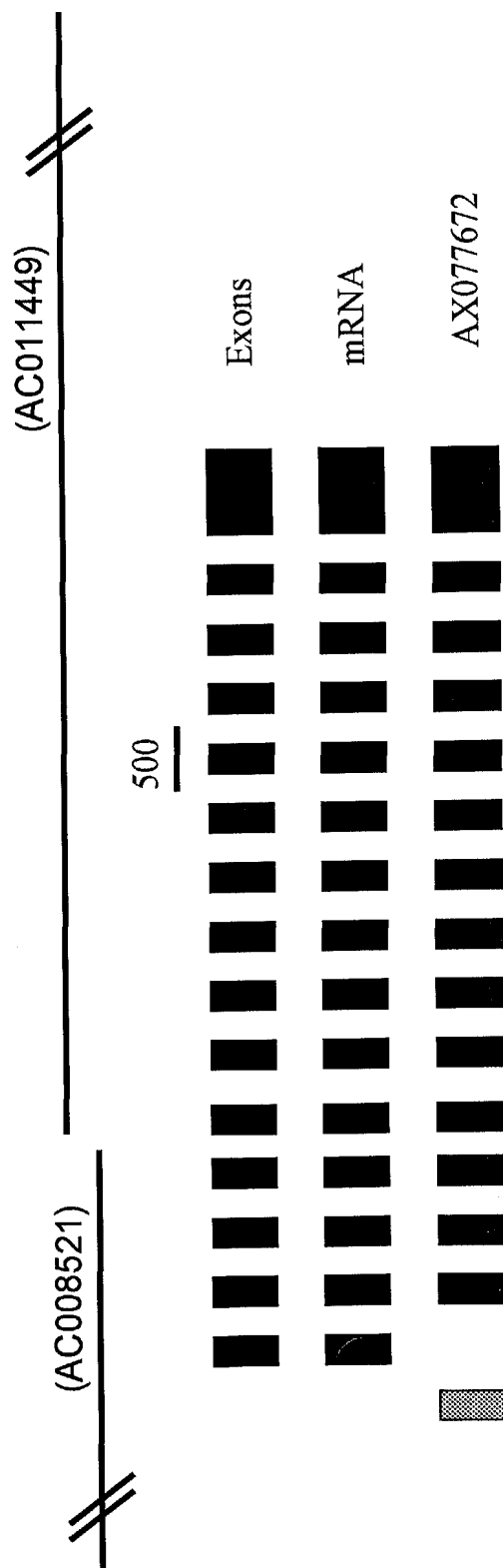


Fig. 3

Nucleotide and protein sequence of the GRBP2 gene

nt: SEQ ID NO: 1

aa: SEQ ID NO: 3

								M	T	D	A	L	L	6
tc	cgc	gcc	cgc	gcc	gct	agc	ATG	ACC	GAC	GCG	CTG	TTG		38
P	A	A	P	Q	P	L	E	K	E	N	D	G		19
CCC	GCG	GCC	CCC	CAG	CCG	CTG	GAG	AAG	GAG	AAC	GAC	GGC		77
Y	F	R	K	G	C	N	P	L	A	Q	T	G		32
TAC	TTT	CGG	AAG	GGC	TGT	AAT	CCC	CTT	GCA	CAA	ACC	GGC		116
R	S	K	L	Q	N	Q	R	A	A	L	N	Q		45
CGG	AGT	AAA	TTG	CAG	AAT	CAA	AGA	GCT	GCT	TTG	AAT	CAG		155
Q	I	L	K	A	V	R	M	R	I	G	A	E		58
CAG	ATC	CTG	AAA	GCC	GTG	CGG	ATG	AGG	ATC	GGA	GCG	GAA		194
N	L	L	K	V	A	T	N	S	K	V	R	E		71
AAC	CTT	CTG	AAA	GTG	GCC	ACA	AAC	TCA	AAG	GTG	CGG	GAG		233
Q	V	R	L	E	L	S	F	V	N	S	D	L		84
CAA	GTG	CGG	CTG	GAG	CTG	AGC	TTC	GTC	AAC	TCA	GAC	CTG		272
Q	M	L	K	E	E	L	E	G	L	N	I	S		97
CAG	ATG	CTC	AAG	GAA	GAG	CTG	GAG	GGG	CTG	AAC	ATC	TCG		311
V	G	V	Y	Q	N	T	E	E	A	F	T	I		110
GTG	GGC	GTC	TAT	CAG	AAC	ACA	GAG	GAG	GCA	TTT	ACG	ATT		350
P	L	I	P	L	G	L	K	E	T	K	D	V		124
CCC	CTG	ATT	CCT	CTT	GGC	CTG	AAG	GAA	ACG	AAA	GAC	GTC		389
D	F	A	V	V	L	K	D	F	I	L	E	H		137
GAC	TTT	GCA	GTC	GTC	CTC	AAG	GAT	TTT	ATC	CTG	GAA	CAT		428
Y	S	E	D	G	Y	L	Y	E	D	E	I	A		150
TAC	AGT	GAA	GAT	GGC	TAT	TTA	TAT	GAA	GAT	GAA	ATT	GCA		467
D	L	M	D	L	R	Q	A	C	R	T	P	S		163
GAT	CTT	ATG	GAT	CTG	AGA	CAA	GCT	TGT	CGG	ACG	CCT	AGC		506

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R	D	E	A	G	V	E	L	L	M	T	Y	F	176
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I	Q	L	G	F	V	E	S	R	F	F	P	P	189
ATC	CAG	CTG	GGC	TTT	GTC	GAG	AGT	CGA	TTC	TTC	CCG	CCC	584
T	R	Q	M	G	L	L	F	T	W	Y	D	S	201
ACA	CGG	CAG	ATG	GGA	CTC	CTG	TTC	ACC	TGG	TAT	GAC	TCT	623
L	T	G	V	P	V	S	Q	Q	N	L	L	L	214
CTC	ACC	GGG	GTT	CCG	GTC	AGC	CAG	CAG	AAC	CTG	CTG	CTG	662
E	K	A	S	V	L	F	N	T	G	A	L	Y	227
GAG	AAG	GCC	AGT	GTC	CTG	TTC	AAC	ACT	GGG	GCC	CTC	TAC	701
T	Q	I	G	T	R	C	D	R	Q	T	Q	A	240
ACC	CAG	ATT	GGG	ACC	CGG	TGC	GAT	CGG	CAG	ACG	CAG	GCT	740
G	L	E	S	A	I	D	A	F	Q	R	A	A	253
GGG	CTG	GAG	AGT	GCC	ATA	GAT	GCC	TTT	CAG	AGA	GCC	GCA	779
G	V	L	N	Y	L	K	D	T	F	T	H	T	266
GGG	GTT	TTA	AAT	TAC	CTG	AAA	GAC	ACA	TTT	ACC	CAT	ACT	818
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CCA	AGT	TAC	GAC	ATG	AGC	CCT	GCC	ATG	CTC	AGC	GTG	CTC	857
V	K	M	M	L	A	Q	A	Q	E	S	V	F	292
GTC	AAA	ATG	ATG	CTT	GCA	CAA	GCC	CAA	GAA	AGC	GTG	TTT	896
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E	V	Y	Q	Q	L	H	A	A	M	S	Q	A	331
GAG	GTC	TAC	CAA	CAG	CTA	CAC	GCA	GCC	ATG	AGC	CAG	GCG	1013
P	V	K	E	N	I	P	Y	S	W	A	S	L	344
CCG	GTG	AAA	GAG	AAC	ATC	CCC	TAC	TCC	TGG	GCC	AGC	TTA	1052
A	C	V	K	A	H	H	Y	A	A	L	A	H	357
GCC	TGC	GTG	AAG	GCC	CAC	CAC	TAC	GCG	GCC	CTG	GCC	CAC	1091
Y	F	T	A	I	L	L	I	D	H	Q	V	K	370
TAC	TTC	ACT	GCC	ATC	CTC	CTC	ATC	GAC	CAC	CAG	GTG	AAG	1130

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GCC	ACA	CTG	AAG	AAT	GAT	CAG	CAG	CGC	CGA	CAG	CTG	GGG	1247
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AAG	TCC	CAC	TTG	CGC	AGA	GCC	ATG	GCT	CAT	CAC	GAG	GAG	1286
S	V	R	E	A	S	L	C	K	K	L	R	S	435
TCG	GTG	CGG	GAG	GCA	AGC	CTC	TGC	AAG	AAG	CTG	CGG	AGC	1325
I	E	V	L	Q	K	V	L	C	A	A	Q	E	448
ATT	GAG	GTG	CTA	CAG	AAG	GTG	CTG	TGT	GCC	GCA	CAG	GAA	1364
R	S	R	L	T	Y	A	Q	H	Q	E	E	D	461
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GAC	CTG	CTG	AAC	CTG	ATC	GAC	GCC	CCC	AGT	GTT	GTT	GCT	1442
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AAA	ACT	GAG	CAA	GAG	GTT	GAC	ATT	ATA	TTG	CCC	CAG	TTC	1481
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GGG	TTC	ACC	TTG	AGA	GGG	AAC	GCC	CCC	GTT	CAG	GTT	CAC	1637
F	L	D	P	Y	C	S	A	S	V	A	G	A	552
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R	E	G	D	Y	I	V	S	I	Q	L	V	D	565
CGG	GAA	GGA	GAT	TAT	ATT	GTC	TCC	ATT	CAG	CTT	GTG	GAT	1715
C	K	W	L	T	L	S	E	V	M	K	L	L	578
TGT	AAG	TGG	CTG	ACG	CTG	AGT	GAG	GTT	ATG	AAG	CTG	CTG	1754

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K	S	F	G	E	D	E	I	E	M	K	V	V	591
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AAG	AAG	CTG	CCC	TCC	cct	ttc	agc	ctt	ctc	aac	tca	gac	2066
S	S	W	Y	*									686
agt	tct	tgg	tac	taa	tgt	gag	gaa	aca	aac	atg	ttc	agg	2105
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cct	gtt	ttt	ctc	ata	gtg	taa	act	cac	att	tga	tgt	gtt	2222
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agg	cag	gtc	aga	gga	ctg	taa	tga	tag	aat	taa	att	agt	2534
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ttt gta ttt tta gtt gag gtg agg ttt cac cat gtt ggc	3119
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aca ccg tga atc taa taa ggt tca ctg ttg aca cag tac	3314
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ctt aaa gga agc aac cac ctt tgg gaa agt gta tct gct	3431
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